Appendix for:

The long noncoding RNA uc.291 controls epithelial differentiation by interfering with ACTL6A/BAF complex

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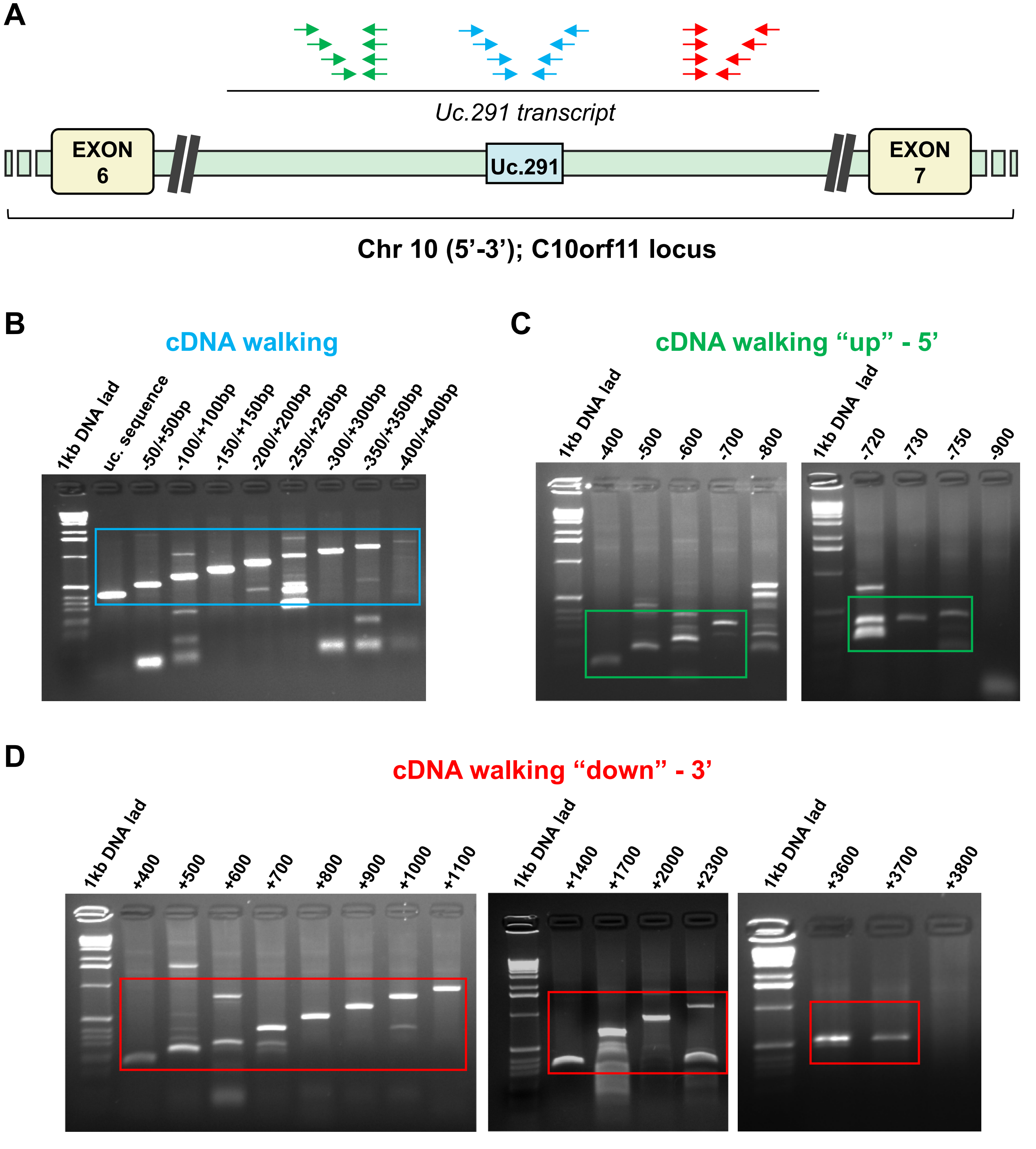

Appendix Figure S1. Characterization of uc.291 transcript by complementary DNA (cDNA) "walking". By using a multiple primers amplification approach we defined the length of uc.291 transcript. Primers were designed on 3' and 5' side of uc.291 conserved sequence at specific distances. "0 bp" represents the amplification of the genomic reported uc.291 length (424 bp in *UCNEbase*). (**A**) Scheme of the walking approach; (**B**) PCR fragments obtained using the blue primers reported in (A); (**C**) PCR fragments obtained using the green primers reported in (a); (**D**) PCR fragments obtained using the red primers reported in (A).

5′ CTGGGCACTTAGCTCTCCACTTTAATTATTCATCCTTATGAAGAAAAATTTCCCCCGTGTGCTTTATTGTCCTCCAGC
CCCGACCTGAGCTCACGCAGACTCTTCCTTCTTTCCCTCCCCAAAGTGGCTTGTGTGTCGAAGGGCTTTCCACTGGGGTG
CTTATTCCATTTATGCCTTTAGTATGCATTTTGTGTTCTGCCAAGGGGGTCAGGAGGGCACATGGAGAAGCCAGATGGCT
TACCTCTTCCCTCAGGAAACACGCCGCTATTTAGCTGGGCACCTTCCCAACTCAAGGCGGGGTGAGATTCCACTGTTGGA
GAGAGAGTTGGTTCAAATGCCACTGTCCCTGAGATCACAGCTCCAAGTTCCTCTAGGCTATGCACTTTTCTACTTCTCTG
CCACTTGCTGGAGTTTTCTGCCAGAAACAGCCTTTTAGGAGATATTAGAAAGGGGGGTGGGAAGGGAGGGATGGGAAAAA
GCAACTCTTGTTATTTATGGTCCTCGTTCAGGCACAAGTTTCTGTTATTTTAATCCGGCTGAAATAAGAAACCATAATCC
ATGGATGAAAAGATGGTGGACAAACTCAGTTAAATCTTGAGCACCCTGAGGATGTGTGTTTTTCCCTATTTCTGGTTTTT
GACGTTCCTTCCCTGCTGCCATTTCCCAACTTTAACTTTTGAAAAGCCAAGCAGTTTGGCTGGCCAGGCCCAGGGAACTT
ATTTGTATGCAGCACAAATTTCAGAATCTGTTCTCAGCCTGTGCCGAGTGAAAAATGGCCTGCATTTTCTTGATAGCCCA
TGTGGTTGTAAAGAATAAATGGCTAATGAATTACAGATGAACATTGACGCAAATTAATCTTCCCGCTGTCCCTGGGTTAT
ATGGCAGCCATTTAAAAGTTTAATCAATACACTAAAGTTGAAAACATGCAGGCACTGCAGTTGTTTGGATGTAATAAACA
TCAGAGGGAACCGGGAGGTTTGCACCCAGTCCATGTATCATAATGACAGGTATTTATGTTTAATGGACTAAATATTTTTT
ATTGGAAGGGAGCAAATGTCAGCTTAACTTTGTGAGCCCCGCATTCAACTTTCCTTTGAGGTTGGTGAAAGACGGCTGAC
GTGTCATTGGAAATGAAATGTTAAGGGAGAAAAAAAGCACAACGGAGACAAAGCGAGGATGGGAGCCGTTTGGAGACGTG
GTGCAGCGCTTACATTCTGCAGCAATTCATTAACGAAAACGTAAACTCTGATATTTCTAATGTTGCTGTAAAATGGTTTA
CTAGGAACAACTTTAATGGTTATTAGTGAAAACAAGTACCCAGATCTGCCAGATATCCTTTTCAGTGCAGGCTTTTGTTT
GAAAACTCTTTACCAGGTCATATTTGCTGGAGATTTATAATTAGTCTTTTTCCTTAATGTGAGAAGTGGAGGAGAAACAG
CGTGATGGCTCTCAGCTCTTGTATTCCATAGATCTTTCCTTTTGAACGGTGTCCAATGACTTCGAATAACCATGTGTTCT
CTTTTGGAATACTTATATCTTAATTACTTTTCAAGTCAATATTTTGTACCTCTGCCGTGAGTCTGGAAGGACCAGGGAGC
TAAAAGAGAAAGGAAATTGCCAGTGGCAGTGCCATCTCGCTGGACAAAAACAGGCTGAGACACAGGAGAGCAATGGCTTC
ACTTGAACAGAAAAATACAGACTTAGTTCAGCTTTTCATTTTTTTTCCTCCACATATAAAATAAACTAAATATGTCAGTG
GAGCATGGGGTCTTAGAAAATAACACACACTTTATAAAAATAATTAGAAACGTTTTAGACAAAGGATATCGTGTTTTTAA
TGTCCCTTCTGCAACCAATTGTCTCAGGTCCTCTTCAGTGTCTGAGGGCACATTCAATGGCAGGGCTTGGAAGAAAATTA
TTCAGTAGATAGCAAGATGAGGCTGAAGGATGAGAAAAAGGGACAGGGGTTGTGATACTTATCCAGTGTTCAGATCTTGC
AAAAGATATGAATTGCACCTTTTTATGTGTTAAATAATTTTGTTAAAATCACAAGAATTTGTGTTTCTAATGGGCCTAAG
TTTCATAGGTAATCAGTATTATGTGATACTAAATTAGTAAACCAAACTGATGGGTTCATTGGTCCTTCATCATCCCTTAA
GCAAAATGGGGAGAAACTTTCTGTTATGAAAACCGAAGCATGGCTCACTGTTAACCATGATGACATCTCACCCACTACTG
CTCCTGAAGTCCTAAACTCTATTTTTCTTCCTACCTCTTTCTACCCTCTTAGAGGATTGAGTCCTTTACCTGTTTGTTCA
CTTTGTGTTTCCGCCGTGTGAATATAAGCTCCACAGTAGGGGGTAGGAGGCAAGAACCTGATTTTCTTCTTTGCTTCTAG
TGTCCTGGGGCCTGGCCTATAATAGGTTCTTGTAAATGGCAGGTAAGTGAATGGCGGACTACATTTCTTATGGTCTTTAG
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TACTTGATCTTAGTTGTTAACTCTAGAAGATAAGAGTTATTATCTTCATTTTATAGAGGCAAAAACTGATGTCAAGAGAA
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TCTAGACTATAACCAGCCAGCTCCCCAACTGGCTGATAATGAACAGAAGTATTAGATTCACAATTTGCAACCTAAACCTG
GTGTCCTGAGTCCTACCTATAGAAAGCAATCTTTGACTGTACAAAAGTAGCACATTGGCTATTTGATGATGGGTGATATG
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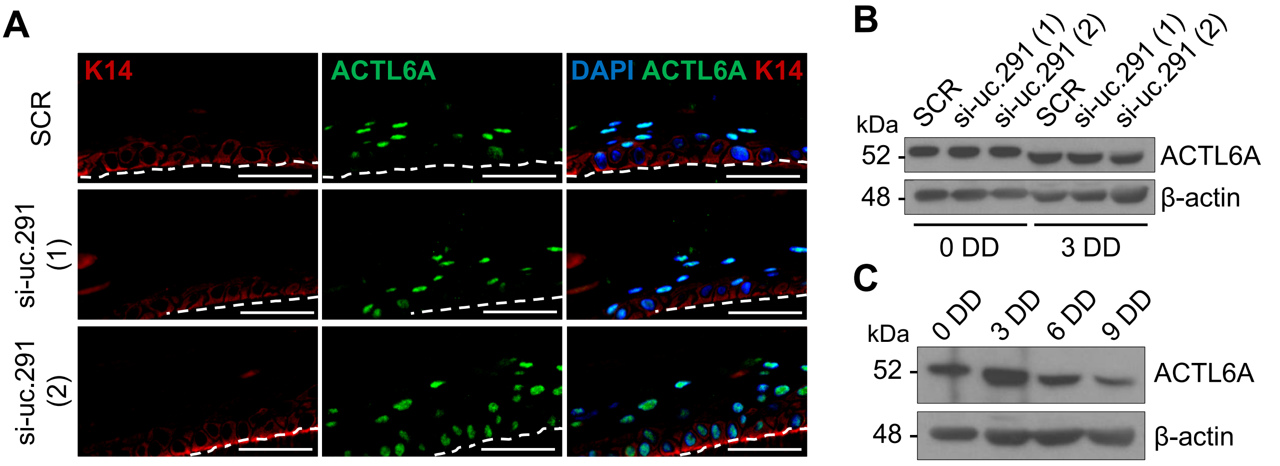
AGTGATAGTGGCTGAAAGAGCAGATCAGTAGGCACCCAGGTCCTTTCTGTCTTTCTGTCCTACTACCTTTTCAGCATGTG
CATTTTAGCCTCATGGTCTCAAAATGGTTGCTACTGCTCCTGGCATCATTTCCTCACCCAAAGCAAGATGAAGAAGGATG
TCTTTCCCTTATGAGGCATTCGCTTTTCATTTGTGGATAGACAGCTTCCTAAAGATGTCTGTCTCTTTCTCATTACCCAG
ATCATGTCATTGGGAGGCTGGAAAGTCAAATGTTTCAGTTTTCATGCTGTTATAGTAGAGGAAGGCAGGATAAAAGGGAG
CCAATGCATAGTGTCTCCTATGTAAGATAAATCGCATTTTTTGTATACCTAATAAAGACTTGAAACTTTGCTAGATGCCA
TATGCACATCAACTTATATCATGTTTACAACCACCTTGTTACAGAAGAGTATTTATTCCCATTACACTAAGAAGAGGTGA
TCTCATTGTTCAATTCCCACCTATGAGTGAGAATATGCGGTGTTTGAAGGGGAATATCACACTCTGGGGACTGTTGTGGG
GTGGGGGGAGGGGGGAGGGATAGATTGGGAGATATACCTAATGCTAGATGACGAGTTAGTGGGTGCAGCGCACCAGCATG
GCACATGTATACATATGTAACCTGCACAATGTGCACGTGTACCCTAAAACGTAAAG 3′

Appendix Figure S2. Uc.291 transcript sequence. Uc.291 complete sequence (3816nt) characterized by cDNA walking followed by sequencing of the PCR fragments obtained. Ultraconserved sequence is in red, predicted ACTL6A binding sequence is in light blu.



Appendix Figure S3. ACTL6A expression during keratinocyte differentiation. (**A**) IF staining of K14 (basal layer marker) and ACTL6A in uc.291-depleted, si-uc.291(1) and si-uc.291(2), organotypic human epidermis compared to scramble control (SCR). Bar: 25um. One representative experiment of three is shown. (**B**) Immunoblot showing ACTL6A protein levels in HEKn cells transfected with scramble sequence (SCR) or si-uc.291(1) and si-uc.291(2) oligos and collected at proliferating (0 day) or differentiating (3 days of differentiation, DD) conditions. β-actin was used as loading control. (**C**) Immunoblot showing ACTL6A protein levels in HEKn cells collected in proliferating (0 day) or differentiating (3, 6, 9 days of differentiation, DD) conditions. β-actin was used as loading control.

Probe for T-UCR	Fold-change	Parametric p-value	FDR	Description
uc.262	6.9380217	5.00E-07	0.0005516	CAGGCTGAGTACAAATTACTATGCAAGGGAGGCTGAGGGT
uc.283	3.9902288	0.003973	0.0439591	CAGGGGCGCGGGATTGGATCAAATCACATAAACTGCAAAA
uc.145A	3.4355936	0.0025296	0.0367763	TCCCATCCACGCGCCTCATACATATTGATTTCTGACACCA
uc.36	2.935153	0.0042701	0.0455497	ACTTTCCTTGTGTGCTTGCACTATAGGTTTGGGACTGACA
uc.88	2.6496588	0.0053214	0.0514358	GGAGGGAAGCAGAAGTCGGGAAGAAAAGAGAAAAGCAGCA
uc.231	2.4696586	0.0142377	0.0922464	TGTGCATGTCAGCAGAATTCATAAGAACTTACAAAATCTT
uc.291A	2.3985146	0.0144979	0.0932284	TGCCATATAACCCAGGGACAGCGGGAAGATTAATTTGCGT
uc.473A	2.2716886	0.0023525	0.035347	CAGACACGGGGAGACACAACAGCACAGAACAGAGAACAAA
uc.220	2.1861354	0.0191878	0.1134554	TCAAGATTTGCCAAACCACTAACCGCATGTATCATTTGCA
uc.339	2.1658364	0.0007872	0.0230286	ACAGGAATGTAATTTTGCCCGGATGAGGCCCCGAGTTTAA
uc.77A	1.9122857	0.0158713	0.0992502	TCTTGGGAGCAGTGTGACAGAAACAGAGTGTGGCGAGAAC
uc.117A	1.8411175	0.0018504	0.0321861	AAACTTGTTTATTAAGATGGGCTGGAGGCGCTGGTGTGCA
uc.170	1.661361	0.0060615	0.0552691	ACACAGGAACAAAGCAAGAGAACAGAAACTCAGAGGCAGA
uc.346	1.6574337	0.0007029	0.0218725	TTCGGAGGCGGCTTTTCTTATTCAAAACAGGCCCACAATG
uc.142A	1.6263274	0.0016429	0.0308253	GTCACACCCGAACCGCCAACAAAATTATCTTAAGCTGCCA
uc.388A	1.5296091	0.0099989	0.0733348	AGCAACACACCATTTCACAGTCTATCGGGCACAAACACAT
uc.20A	1.4471174	0.0436931	0.2063864	CTTGGTGAGGTTTGGGCGGAATAAAGAAAGGTGTTGGTGG
uc.110	1.4082587	0.0031046	0.0398286	ACAAGTTGCTGTTAATTTAGTGCAGGGAGGACGGGATGGA
uc.398A	1.3920305	0.0497388	0.2267608	GGATCGGGAGGAGGAGAGCCAGCGACCACAAAGAAGACAG
uc.478	1.3431458	0.0239285	0.1326632	AAACAAATGGTGGTACGACAAAGGAGAGTGCGGCAGCGGG
uc.217A	1.276802	0.021647	0.1232889	AAAGCACCCTTCACAAAGCCACAAACAAGAAGCAGGACAG
uc.208A	1.2115439	0.0348729	0.1738692	TCAATGAAGAATGAAGAGAAGTAGAAAGCAAGAGTGAAGT
uc.310A	0.65047	0.0210915	0.1214111	GGCCTGTCTCTCCTCTTCTTTTTCAAACCAAATTCTGCTT
uc.369	0.6353444	0.0467179	0.2170893	TGATCTCATATTAAATTTTCCCCTGAATCCGCCCCTTGGC
uc.198	0.6342153	0.0182638	0.1091729	CTGGTGACAAGTGAAATTGCTGTGCGCCTCATTTAGCTGT
uc.262A	0.6117229	0.0442415	0.2085941	ACCCTCAGCCTCCCTTGCATAGTAATTTGTACTCAGCCTG
uc.16	0.6081178	0.0409966	0.1964124	CTTGTTCAACACAGAGCTTAGAAACCCTCCTTCCACTCCC
uc.478A	0.5942682	0.0280721	0.1492947	CCCGCTGCCGCACTCTCCTTTGTCGTACCACCATTTGTTT
uc.352	0.5837183	0.0263843	0.1424184	TTTAAAGGCCAAGTCTAAAATAGATTTGCACCCACGCCCC
uc.242	0.5766099	0.0308061	0.1585047	TTTAGTAGTTCCGCTATTCTGCTTAACATGTGGCACCCGT
uc.138	0.5757989	0.0400969	0.1932085	CTGACTTCTTTCATCTTCCCCACTTCACACAAATTGCTCA
uc.28	0.5717847	0.0282912	0.149858	AACTATATACCAGGCCCTGCTGAAAATACCACCCAACAGT
uc.462	0.5621613	0.0064514	0.0572034	GGTGGGTGGAGAGACGAAGTCAGGGCTGTTTGTTGAATAT
uc.452	0.5604607	0.0385909	0.1877993	AGCGTGTTTCTAATGCTATTCACCTGCCTTTGATGATTGA
uc.346A	0.5596938	0.0026415	0.0374468	CATTGTGGGCCTGTTTTGAATAAGAAAAGCCGCCTCCGAA
uc.325	0.5579312	0.0104034	0.0750892	GGGGTTTTGTTGTCAGAGTAGTTCCCGCCTCATGTTTTGT
uc.151A	0.5475617	0.0166494	0.1023798	TCTTGCTCACCTGGTCAAACACCCATTCCTCACTGCATTT
uc.390	0.5450069	0.0322261	0.1638461	AATTTAGTCAATTACTGTTTCAGCCTGCAAGCCTCCTGGG
uc.396	0.5407496	0.0161342	0.1001554	CATCTTGCACAGCTGCGCCCAACTGATTAAATCCTCACAA
uc.77	0.5379875	0.0382952	0.1867631	GTTCTCGCCACACTCTGTTTCTGTCACACTGCTCCCAAGA
uc.412A	0.5237442	0.031904	0.1631937	TTCAAATCCACACAAGCCTGCCACTTGCACTAGTCATCCC
uc.21A	0.5211857	0.0325936	0.1651708	ACCCATAATTTCTCATTTCCCAAACCTCACACATGCTGAA
uc.465A	0.5019852	0.0026524	0.0374468	TTCTCTCATCTCCCGCAGCTTAGCACCTGTCTTTGTTTGG
uc.400A	0.497497	0.0270436	0.1454441	AATCATCTGACACAAAGATAATTGAGCCAGCCTCTGCCAC
uc.457	0.496534	0.0180181	0.1085937	AGACATATTCCAGATCACAACCTTCCCAGAATCCTGCCCT
uc.268	0.4928927	0.0027834	0.0383176	ACTATCATCACAACCCTCATTGTTCCATCTCTGCCCTCCC
uc.129	0.4880591	0.0251525	0.1374754	CCATTGCCATCATGTGCTCGCTGCCTGCTAATTAAGACTC
uc.223A	0.4698592	0.0008607	0.0242558	GGCTGATTTATGTTGTCATTCCCTCTCACCAGTCCTGCAT
uc.373A	0.46421	0.0193354	0.1138975	TTGAAAGGAGACAACATTGTCCCGATTTCCCACTGCGACA
uc.473	0.4634708	0.0022747	0.03482	TTTGTTCTCTGTTCTGTGCTGTTGTGTCTCCCCGTGTCTG
uc.133A	0.4487399	0.0259639	0.1407152	ACTTTCCGATTTAATTTCCTCCATGCCCTTGACATCCACA
uc.476A	0.4466684	0.0276283	0.1476632	GCTGATTGATGGCTCTCTCCCTCACTGCTGAAGGCTGTAT
uc.422	0.4430617	0.0099478	0.0730988	GAGATTCTGCATTACTACACCTCAGTGCCTGCCTGGTTCC
uc.250	0.4364047	0.0070389	0.0603978	GCAAATATGATTATACACTATCAAACTGGCACCACCAGGC
uc.10A	0.4228508	0.0180147	0.1085937	TCTGCATCTCCTAATGGCCTCTGCTCCTCTACACTCAATT

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uc.335A	0.4227937	0.0146008	0.0936515	CAGCAGAAGCAGGTCTCAGGTCCCAGTGGTTAATGTAGTG
uc.281A	0.4197648	0.0082006	0.0648906	GCCTTTATTGGAATTCTGAAACCTCTCTGCCTCCCTGGCT
uc.391A	0.4037248	0.0289005	0.1520426	AAATTATTGCATTGCTGGTGGCAATTTGTGGGCATGTGTT
uc.305A	0.3992737	0.0028265	0.0385672	CGGCAGGCTCTTCCCATCTTCCCATCCATTCATCATCTCG
uc.161A	0.3980419	0.0007734	0.0228909	CCATCATAATTTGTTCATTTGGTGCCCATCAGCCCAGCCT
uc.177A	0.3960284	0.048816	0.224542	CACAATTTCAAAACTGCCTGCTAATTTCCACCACCTGTCA
uc.159A	0.3946312	0.0031571	0.0401024	GGTCCTCCACAGTCCCAAATTCACCCGTTTAAGCCATAAT
uc.416A	0.3747073	0.0023867	0.0355154	GCTGCCATGCACACCGGCTCTTACGGCTACAATTACAATG
uc.134A	0.3737976	0.0088282	0.0679086	GCTCATAAATTACTGCTCTTTTGTTGCTGGCTGGCCTTGT
uc.1	0.3736053	0.0064382	0.0571786	CACTTCCCCACCGCAGGCTTTGCTGAGCAGTTTTAGTATC
uc.181A	0.3669021	0.0016712	0.0308772	GAATGAGCAGGCCCCAAGGTGTTTCAACTGGAGTGTTTTC
uc.349	0.3633513	0.003553	0.0415567	ATGTTTTCCACAGCCCAAGACCTTTGGTGCATGCTTTTGA
uc.266A	0.3471284	0.0207761	0.1199206	AGACCACTTCAATTTCAGCTTCTGCCAGCCTCGTTTGAGA
uc.136	0.3449797	0.0143047	0.0925777	CAATAACGCTTTGATAGATCCCTGTCTGCCCGGTGCTTGA
uc.411	0.3341136	0.0003292	0.0146432	ACCCATTTGTCACCCAGCATTTCCCTTTGTGTATAGAACA
uc.164A	0.3221855	0.0045111	0.0470165	TTACCACATGCTGTCACAGTTAGCTCAGCCAGGTCTTGTT
uc.329A	0.2860004	0.0025932	0.0370876	TGTAGTCATCAAGTGAGAAAGACATCCTCCTCCTGGCTGC
uc.232	0.2818089	0.0006993	0.0218725	AAGTGTTGTGTCAATAACGCAGCCAAGATCTCGCCAATCG
uc.63A	0.2714599	0.0012258	0.0280916	CAGTGTTTGCCTGTTTGCTTGCCTGGTAAATTTTGCTTTT
uc.257	0.2624234	0.0002364	0.0124403	CTGATGGATTCCCAGGCCCATTGCTGTCACTGATGAACTA
uc.338A	0.2565722	0.0010626	0.026549	CTGTCGCTGCCTGTGCTGTACCTGTCCTGTGGATAAATAG
uc.183A	0.250974	6.32e-05	0.0068978	CCCAGTGTCAGATGTCTCCAGGTGCCTCTCTTCTTTCTTG
uc.252A	0.2239623	0.0002429	0.01259	TCTCAGGAAGCCCAGCCAATTAAGGACTTGACCATATTGA
uc.204A	0.1862553	2.7e-06	0.001604	GCTCTAATTTACAAGCCGCCTGCCTAATGAATTGTCTGGG

Appendix Table S1. Modulated T-UCRs during keratinocytes differentiation

Description:

Number of classes: 2

Type of univariate test used: Two-sample T-test

Nominal significance level of each univariate test: 0.05

Summary of Results

Sorted by p-value of the univariate test.

Class 1: differentiated; Class 2: undifferentiated.

The genes are significant at the nominal 0.05 level of the univariate test

Gene Symbol	Expressed in epidermis*
BATF2	yes
SMARCE1	yes
ACTL6A	yes
TRIM16	yes
TADA2A	
CENPO	
DEK	yes
CRTC2	yes
UBE2B	
BRCC3	
CHCHD3	
SETMAR	
CHD2	
SMARCC2	yes
VEGFA	yes
PRMT3	yes
C17orf49	yes
GATA2	
MRGBP	
BMI1	yes
CPA4	yes
PRMT6	yes
CHCHD2	yes
DCAF17	
SMARCD3	
SETDB1	
EYA1	
UBE2U	
ZCRB1	
GATA3	yes
EPC1	
PRKD2	yes
ATXN7L3	yes
HJURP	
CENPA	yes
SIRT1	
PRKCA	
HIST1H1C	yes
ZNF451	
PHLDB1	yes

Appendix Table S2. List of ranked candidates interacting with uc.291.
Table showing the top 40 uc.291 interactors derived from the protoarray. See also Figure 4 and Figure EV4. * The expression in human epidermis was extrapolated from *The Human Protein Atlas* (http://www.proteinatlas.org).

cDNA Walking	
Name	*Sequence 5'-3'*
F-50	TTCCCAACTTTAACTTTTGAAAAGC
R+475	AAACGGCTCCCATCCTCGCTTTG
F-100	ATGTGTGTTTTTCCCTATTTCTGG
R+525	CGTTTTCGTTAATGAATTGCTGCAG
F-150	GGATGAAAAGATGGTGGACAAAC
R+575	AGTTGTTCCTAGTAAACCATTTTAC
F-200	CACAAGTTTCTGTTATTTTAATCCG
R+625	AAAGGATATCTGGCAGATCTGGG
F-250	AGGGAGGGATGGGAAAAAGCAAC
R+675	TCCAGCAAATATGACCTGGTAAAG
F-300	GTTTTCTGCCAGAAACAGCCTTTTAG
R+725	GCTGTTTCTCCTCCACTTCTCAC
F-350	CCAAGTTCCTCTAGGCTATGCAC
R+775	CACCGTTCAAAAGGAAAGATCTATG
F-400	CTGTTGGAGAGAGAGTTGGTTC
R+825	AAGATATAAGTATTCCAAAAGAGAAC
cDNA Walking UP	
Name	*Sequence 5'-3'*
R5'-UP	GGCTGTTTCTGGCAGAAAACTCC
F-456	CGCCGCTATTTAGCTGGGCACC
F-505	GGAGGGCACATGGAGAAGCCAG
F-620	CAGACTCTTCCTTCTTTCCCTC
F-647	GTCCTCCAGCCCCGACCTGAGC
F-685	CATCCTTATGAAGAAAAATTTCCC
F-715	CTGGGCACTTAGCTCTCCAC
F-732	AACTACAGTGAGGCCTGGGCAC
F-861	GAGTTGCTGCCTTGTACAGCTG
cDNA Walking DOWN	
Name	*Sequence 5'-3'*
F3'-DOWN	CTTTACCAGGTCATATTTGCTGG
R+875	TCCTTCCAGACTCACGGCAGAGG
R+923	GCGAGATGGCACTGCCACTGGC
R+1060	CTAAGACCCCATGCTCCACTGAC
R+1177	AATGTGCCCTCAGACACTGAAG
R+1288	CTTTTGCAAGATCTGAACACTGG
R+1440	GGGATGATGAAGGACCAATGAAC
R+1578	CTTCTAAGAGGGTAGAAAGAGG
F3'-1500-DOWN	CCCACTACTGCTCCTGAAGTCC
R+1826	CAACTAACAGAGTGACTAGAAATC
R+2118	CAGCCAGTTGGGGAGCTGGCTGG
R+2400	CCTGGGCTGCCTACCTCCATTC
R+2664	CCAGCCTCCCAATGACATGATC
F3-2700-DOWN	GGATGTCTTTCCCTTATGAGGC
R+3040	CTGGTGCGCTGCACCCACTAAC
R+3100	CTTTACGTTTTAGGGTACACGTG
R+3200	GTCAGACCTGATAATTTAGGGC

Appendix Table S3. Primers list used in the cDNA walking experiment (see also Appendix Figure S1).

Name	*Sequence 5'-3'*
T-UC291 FW	GCGTCAATGTTCATCTGTAATTC
T-UC291 REV	CTGTTCTCAGCCTGTGCCGAG
T-UC183 FW	TGCTTCTTCTCTTCCTTCCTTTTTG
T-UC183 REV	TGCTCTCTACCAGGTTGGCG
T-UC257 FW	GCTGATGGATTCCCAGGCCCATTG
T-UC257 REV	GTTCTGATCTTGAGGTAATTAGCC
T-UC338 FW	AGTGAGCCTTGGAGACTGAACATCC
T-UC338 REV	ACAGCCCTGGAGACTGAAATCCTC
T-UC63 FW	CAGTGTTTGCCTGTTTGCTTGC
T-UC63 REV	CCTGTTGCTTTCTTTCTGTTCCTC
T-UC36 FW	AAATGTGTGTGAGTGCAAGCAG
T-UC36 REV	GGGTCATTACCGCATGAAGGCC
T-UC88 FW	TGTCAAAACTGCCAGGAGCAAG
T-UC88 REV	GCCAATCTGTCACCGTTCAGC
IVL FW	CAGGTCCAAGACATTCAACC
IVL REV	CAAGTTCACAGATGAGACGG
KRT10 FW	AGGAGGAGTGTCATCCCTAAG
KRT10 REV	AAGCTGCCTCCATAACTCCC
LOR FW	CTCTGTCTGCGGCTACTCTG
LOR REV	CACGAGGTCTGAGTGACCTG
U6 FW	GTGCTCGCTTCGGCAGCACATATAC
U6 REV	AAAAATATGGAACGCTTCACGAATTT
ACTIN FW	GTTGCTATCCAGGCTGTGC
ACTIN REV	AATGTCACGCACGATTTCCCG
LCE1B FW	GCTACAACTACACTAAGCAGTTC
LCE1B REV	CTATTCTTGCCCTTTCAGCATCA
LCE1C FW	AATCCAGGACCGCAAACTG
LCE1C REV	TGGACCTGTGAGCCTCTCAG
LCE2B FW	GGTTGACTAAACTCTGCCAGG
LCE2B REV	GGCACTGGGGCAGGCATTTA
LCE2D FW	CTGCAGAAGAGCTCTGGTACTG
LCE2D REV	CTCCATCAAGCACAAAGTTCTG
LCE3A FW	CTGAGTCACCACAGATGCC
LCE3A REV	CTTGCTGACCACTTCCCCTG
LCE3C FW	CCAGTTGTCCCTCACCCAAG
LCE3C REV	CCGGAGCTTAGAGCACAGTC
LCE6A FW	CAGGGAGCTGAAAAGCCAGA
LCE6A REV	GAGGGGAGCATTTGGGAACA
SPRR2B FW	AGGAACCTTGGCTTTGTCAGT
SPRR2B REV	AGCTCATGCCCAGGTGAAAG
KPRP FW	CCTGAAGGACTGCTTGCCTG
KPRP REV	CTGGGCAAAGGGGGATTGAG
HRNR FW	GAAGTGCTCAGGGCAAGAT
HRNR REV	GCACCTCTGCTCTTGGACAT
FLG FW	CAATCAGGCACTCATCACAC
FLG REV	ACTGTTAGTGACCTGACTACC
TBP FW	TCAAACCCAGAATTGTTCTCCTTAT
TBP REV	CCTGAATCCCTTTAGAATAGGGTAGA

Appendix Table S4. Primers list used in the RT-qPCR

Name	*Sequence 5'-3'*
LOR FW	TCTCCTTTCCTGCATTCGCT
LOR REV	TTCGTTTGCCAGCCATTCCT
FLG FW	CCAAGGCAAAGGGCAAGATTC
FLG REV	GCTACGCTGTCTAGCTCTCTG
LCE1B FW	TGAAGGAGGGAGCCTCAAGA
LCE1B REV	TACAGGTGAACATGGCAGGC
TBP FW	CTGACAGGTAAGGAGGACGC
TBP REV	AGTTACCTGACCTCTCCCCC

Appendix Table S5. Primers list used in the ChIP experiments (see also Figure 5).